



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/762224
Source: PCT09
Date Processed by STIC: 09/24/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-42
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,224

DATE: 09/24/2001
TIME: 15:58:37

Input Set : A:\Seq List-Pur-115.txt
Output Set: N:\CRF3\09242001\I762224.raw

W--> 1 PUR-115:JJS:133252
5 <110> APPLICANT: Sanders, David A.
6 Kuhn, Richard John
7 Jeffers, Scott A.
8 Sharkey, Curtis Matthew
9 North, Cynthia Lin
10 Fishbach, Michael A.
12 <120> TITLE OF INVENTION: PSEUDOTYPED RETROVIRUSES AND STABLE CELL LINES FOR THEIR
PRODUCTION
14 <130> FILE REFERENCE: 7024-497/PUR-115
16 <140> CURRENT APPLICATION NUMBER: US 09/762,224
18 <141> CURRENT FILING DATE: 2001-02-02
20 <150> PRIOR APPLICATION NUMBER: PCT/US99/17702
22 <151> PRIOR FILING DATE: 1999-08-04
24 <150> PRIOR APPLICATION NUMBER: U.S. 60/095,242
26 <151> PRIOR FILING DATE: 1998-08-04
28 <150> PRIOR APPLICATION NUMBER: U.S. 60/112,405
30 <151> PRIOR FILING DATE: 1998-12-15
32 <160> NUMBER OF SEQ ID NOS: 3
34 <170> SOFTWARE: Microsoft Word 97

Does Not Comply
Corrected Diskette Needed

Errored:
Field 211 indicates 2176
nucleotides. Found 2224.

Errored from line 372 - integer end total indicates
757 nucleotides. There are 727 nucleotides at
the end of line 368 and 48 nucleotides in line 379.
 $48 + 727 = 775 \neq 757$ Therefore your
end total is $2176 + 48 = 2224$ nucleotides

ERRORED SEQUENCES

301 <210> SEQ ID NO: 2	2	55
303 <211> LENGTH: 2176	2176	
305 <212> TYPE: DNA		
307 <213> ORGANISM: Filovirus Ebola virus, subtype Zaire		
309 <400> SEQUENCE: 2		
312 caacaacaca atg ggc gtt aca gga ata ttg cag tta cct cgt gat cga ttc aag		55
313 Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys		
314 1 5 10 15		
316 agg aca tca ttc ttt ctt tgg gta att atc ctt ttc caa aga aca ttt		103
317 Arg Thr Ser Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe		
318 20 25 30		
320 tcc atc cca ctt gga gtc atc cac aat agc aca tta cag gtt agt gat		151
321 Ser Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp		
322 35 40 45		
324 gtc gac aaa cta gtt tgt cgt gac aaa ctg tca tcc aca aat caa ttg		199
325 Val Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu		
326 50 55 60		
328 aga tca gtt gga ctg aat ctc gaa ggg aat gga gtt gca act gac gtg		247
329 Arg Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val		
330 65 70 75		
332 cca tct gca act aaa aga tgg ggc ttc agg tcc ggt gtc cca cca aag		295
333 Pro Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys		
334 80 85 90 95		
336 gtg gtc aat tat gaa gct ggt gaa tgg gct gaa aac tgc tac aat ctt		343

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337	Val	Val	Asn	Tyr	Glu	Ala	Gly	Glu	Trp	Ala	Glu	Asn	Cys	Tyr	Asn	Leu	
338					100					105				110			391
340	gaa	atc	aaa	aaa	cct	gac	ggg	agt	gag	tgt	cta	cca	gca	gcg	cca	gac	
341	Glu	Ile	Lys	Lys	Pro	Asp	Gly	Ser	Glu	Cys	Leu	Pro	Ala	Ala	Pro	Asp	
342					115					120				125			439
344	ggg	att	cgg	ggc	ttc	ccc	cgg	tgc	cgg	tat	gtg	cac	aaa	gta	tca	gga	
345	Gly	Ile	Arg	Gly	Phe	Pro	Arg	Cys	Arg	Tyr	Val	His	Lys	Val	Ser	Gly	
346					130					135				140			487
348	acg	gga	ccg	tgt	gcc	gga	gac	ttt	gcc	ttc	cat	aaa	gag	ggt	gct	ttc	
349	Thr	Gly	Pro	Cys	Ala	Gly	Asp	Phe	Ala	Phe	His	Lys	Glu	Gly	Ala	Phe	
350					145					150				155			535
352	ttc	ctg	tat	gat	cga	ctt	gct	tcc	aca	gtt	atc	tac	cga	gga	acg	act	
353	Phe	Leu	Tyr	Asp	Arg	Leu	Ala	Ser	Thr	Val	Ile	Tyr	Arg	Gly	Thr	Thr	
354					160					165				170			175
356	ttc	gct	gaa	ggt	gtc	gtt	gca	ttt	ctg	ata	ctg	ccc	caa	gct	aag	aag	
357	Phe	Ala	Glu	Gly	Val	Val	Ala	Phe	Leu	Ile	Leu	Pro	Gln	Ala	Lys	Lys	
358					180					185				190			583
360	gac	ttc	ttc	agc	tca	cac	ccc	ttg	aga	gag	ccg	gtc	aat	gca	acg	gag	
361	Asp	Phe	Phe	Ser	Ser	His	Pro	Leu	Arg	Glu	Pro	Val	Asn	Ala	Thr	Glu	
362					195					200				205			679
364	gac	ccg	tct	agt	ggc	tac	tat	tct	acc	aca	att	aga	tat	cag	gct	acc	
365	Asp	Pro	Ser	Ser	Gly	Tyr	Tyr	Ser	Thr	Thr	Ile	Arg	Tyr	Gln	Ala	Thr	
366					210					215				220			727
368	ggt	ttt	gga	acc	aat	gag	aca	gag	tac	ttg	ttc	gag	gtt	gac	aat	ttg	
369	Gly	Phe	Gly	Thr	Asn	Glu	Thr	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Asn	Leu	
370					225					230				235			757
E-->	372	acc	tac	gtc	caa	ctt	gaa	tca	aga	ttc	aca	cca	cag	ttt	ctg	ctc	cag
	373	Thr	Tyr	Val	Gln	Leu	Glu	Ser	Arg	Phe	Thr	Pro	Gln	Phe	Leu	Gln	
	374				240					245				250			255
E-->	376	ctg	aat	gag	aca	ata	tat	aca	agt	ggg	aaa	agg	agc	aat	acc	acg	gga
	377	Leu	Asn	Glu	Thr	Ile	Tyr	Thr	Ser	Gly	Lys	Arg	Ser	Asn	Thr	Gly	
	378				260					265				270			823
E-->	380	aaa	cta	att	tgg	aag	gtc	aac	ccc	gaa	att	gat	aca	aca	atc	ggg	gag
	381	Lys	Leu	Ile	Trp	Lys	Val	Asn	Pro	Glu	Ile	Asp	Thr	Ile	Gly	Glu	
	382				275					280				285			871
E-->	384	tgg	gcc	ttc	tgg	gaa	act	aaa	aaa	aac	ctc	act	aga	aaa	att	cgc	agt
	385	Trp	Ala	Phe	Trp	Glu	Thr	Lys	Lys	Asn	Leu	Thr	Arg	Lys	Ile	Arg	Ser
	386				290					295				300			919
E-->	388	gaa	gag	ttg	tct	tcc	aca	gtt	gta	tca	aac	gga	gcc	aaa	aac	atc	agt
	389	Glu	Glu	Leu	Ser	Phe	Thr	Val	Val	Ser	Asn	Gly	Ala	Lys	Asn	Ile	Ser
	390				305					310				315			967
E-->	392	ggt	cag	agt	ccg	gcg	cga	act	tct	tcc	gac	cca	ggg	acc	aac	aca	aca
	393	Gly	Gln	Ser	Pro	Ala	Arg	Thr	Ser	Ser	Asp	Pro	Gly	Thr	Asn	Thr	Thr
	394				320					325				330			1015
E-->	396	act	gaa	gac	cac	aaa	atc	atg	gct	tca	gaa	aat	tcc	tct	gca	atg	gtt
	397	Thr	Glu	Asp	His	Lys	Ile	Met	Ala	Ser	Glu	Asn	Ser	Ser	Ala	Met	Val
	398				340					345				350			1063
E-->	400	caa	gtg	cac	agt	caa	gga	agg	gaa	gct	gca	gtg	tcg	cat	cta	aca	acc
	401	Gln	Val	His	Ser	Gln	Gly	Arg	Glu	Ala	Ala	Val	Ser	His	Leu	Thr	Thr

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402	355	360	365	
E--> 404	ctt gcc aca atc tcc acg agt ccc caa tcc ctc aca acc aaa cca ggt			1111
405	Leu Ala Thr Ile Ser Thr Ser Pro Gln Ser Leu Thr Thr Lys Pro Gly			
406	370	375	380	
E--> 408	ccg gac aac agc acc cat aat aca ccc gtg tat aaa ctt gac atc tct			1159
409	Pro Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp Ile Ser			
410	385	390	395	
E--> 412	gag gca act caa gtt gaa caa cat cac cgc aga aca gac aac gac agc			1207
413	Glu Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Asp Ser			
414	400	405	410	415
E--> 416	aca gcc tcc gac act ccc tct gcc acg acc gca gcc gga ccc cca aaa			1255
417	Thr Ala Ser Asp Thr Pro Ser Ala Thr Ala Ala Gly Pro Pro Lys			
418	420	425	430	
E--> 420	gca gag aac acc aac acg aag agc act gac ttc ctg gac ccc gcc			1303
421	Ala Glu Asn Thr Asn Thr Ser Lys Ser Thr Asp Phe Leu Asp Pro Ala			
422	435	440	445	
E--> 424	acc aca aca agt ccc caa aac cac agc gag acc gct ggc aac aac aac			1351
425	Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn			
426	450	455	460	
E--> 428	act cat cac caa gat acc gga gaa gag agt gcc agc agc ggg aag cta			1399
429	Thr His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu			
430	465	470	475	
E--> 432	ggc tta att acc aat act att gct gga gtc gca gga ctg atc aca ggc			1447
433	Gly Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly			
W--> 434	485	490	495	500
E--> 436	ggg aga aga act cga aga gaa gca att gtc aat gct caa ccc aaa tgc			1495
437	Gly Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys			
W--> 438	505	510	515	
E--> 440	aac cct aat tta cat tac tgg act act cag gat gaa ggt gct gca atc			1543
441	Asn Pro Asn Leu His Tyr Trp Thr Gln Asp Glu Gly Ala Ala Ile			
W--> 442	520	525	530	
E--> 444	gga ctg gcc tgg ata cca tat ttc ggg cca gca gcc gag gga att tac			1591
445	Gly Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr			
W--> 446	535	540	545	
E--> 448	ata gag ggg cta atg cac aat caa gat ggt tta atc tgt ggg ttg aga			1639
449	Ile Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg			
W--> 450	550	555	560	
E--> 452	cag ctg gcc aac gag acg act caa gct ctt caa ctg ttc ctg aga gcc			1687
453	Gln Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala			
W--> 454	565	570	575	580
E--> 456	aca act gag cta cgc acc ttt tca atc ctc aac cgt aag gca att gat			1735
457	Thr Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp			
W--> 458	585	590	595	
E--> 460	tcc ttg ctg cag cga tgg ggc ggc aca tgc cac att ctg gga ccg gac			1783
461	Phe Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp			
W--> 462	600	605	610	
E--> 464	tgc tgt atc gaa cca cat gat tgg acc aag aac ata aca gac aaa att			1831
465	Cys Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile			
W--> 466	615	620	625	

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E--> 468 gat cag att att cat gat ttt gtt gat aaa acc ctt ccg gac cag ggg	1879
469 Asp Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly	
W--> 470 630 635 640	
E--> 472 gac aat gac aat tgg tgg aca gga tgg aga caa tgg ata ccg gca ggt	1927
473 Asp Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly	
W--> 474 645 650 655 660	
E--> 476 att gga gtt aca ggc gtt ata att gca gtt atc gct tta ttc tgt ata	1975
477 Ile Gly Val Thr Gly Val Ile Ala Val Ile Ala Leu Phe Cys Ile	
W--> 478 665 670 675	
E--> 480 tgc aaa ttt gtc ttt tag tttttttca gattgcttca tgaaaaagct cagcctcaaa	2033
481 Cys Lys Phe Val Phe	
W--> 482 680	
E--> 484 tcaatgaaac caggatttaa ttatatggat tacttgaatc taagattact tgacaaatga	2093
E--> 486 taatataata cactggagct ttaaacatag ccaatgtgat tctaactcct ttaaactcac	2153
E--> 488 agttaatcat aaacaaggtt tga	2176

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/762,224

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Input Set : A:\Seq List-Pur-115.txt
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L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:372 M:254 E: No. of Bases conflict, LENGTH:Input:757 Counted:775 SEQ:2
M:254 Repeated in SeqNo=2
L:384 M:112 C: (48) String data converted to lower case,
L:434 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:438 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:442 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:446 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:462 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:466 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:474 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:478 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:488 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2176 Found:2224 SEQ:2
L:544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:548 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:552 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:568 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:572 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:576 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:580 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:584 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:588 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:592 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:596 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:600 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:604 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:608 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:612 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:616 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:620 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:624 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:628 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:632 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:636 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:640 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:644 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:648 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:652 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:656 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:660 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

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L:664 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:668 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:672 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3